

SEQUENCE LISTING

<110> Zheng, Peizhong
Li, Chun Ping
Nichols, Scott E.

<120> Oar Polynucleotides, Polypeptides and
Their Use in PHA Production in Plants

<130> 35718/241887

<150> 60/258,417

<151> 2000-12-27

<160> 10

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<212> DNA

<213> Zea mays

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<221> CDS

<222> (157)...(1110)

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ctctctcttg gctctcttgc gtcccgacgc ccctc atg gcc acc gcc gcc gcc 174
                                     Met Ala Thr Ala Ala Ala
                                     1                               5
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acc gca gca gca gca gca gtc tcc tcc ccg gct gcg cgt gga gca gcc 222
Thr Ala Ala Ala Ala Ala Val Ser Ser Pro Ala Ala Arg Gly Ala Ala
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Gly Ala Ala Ala Ala Ser Arg Arg Gly Phe Val Thr Phe Gly Gly Gly
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gcc gcc cgc ttc tct ccc acg ctg cgg tcc gcc cgt ggg ttc tct ggt 318
Ala Ala Arg Phe Ser Pro Thr Leu Arg Ser Gly Arg Gly Phe Ser Gly
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90 95 100	
ctg gta aac tat gcc cgg tcc tgc aaa gag gct gaa gag gtc tcc aaa Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu Ala Glu Glu Val Ser Lys	510
105 110 115	
gag att gaa gca tct ggt ggt gag gct atc acc ttc gga gga gat gtt Glu Ile Glu Ala Ser Gly Gly Glu Ala Ile Thr Phe Gly Gly Asp Val	558
120 125 130	
tca aaa gaa gct gat gta gag tct atg atg aaa gca gct cta gat aaa Ser Lys Glu Ala Asp Val Glu Ser Met Met Lys Ala Ala Leu Asp Lys	606
135 140 145 150	
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155 160 165	
aca ttg ttg atg agg atg aag aaa tct cag tgg caa gac gta att gat Thr Leu Leu Met Arg Met Lys Lys Ser Gln Trp Gln Asp Val Ile Asp	702
170 175 180	
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185 190 195	
atg atg aaa aag aga aag gga aaa att atc aac att gca tct gta gtt Met Met Lys Lys Arg Lys Gly Lys Ile Ile Asn Ile Ala Ser Val Val	798
200 205 210	
ggg ctt act ggc aat gtt ggc caa gct aat tat agc gca gcc aag gct Gly Leu Thr Gly Asn Val Gly Gln Ala Asn Tyr Ser Ala Ala Lys Ala	846
215 220 225 230	
gga gtg att ggt ttc aca aaa aca gtt gcc agg gag tat gca agc aga Gly Val Ile Gly Phe Thr Lys Thr Val Ala Arg Glu Tyr Ala Ser Arg	894
235 240 245	
aat atc aat gtg aat gct att gca cca ggg ttc att gca tct gat atg Asn Ile Asn Val Asn Ala Ile Ala Pro Gly Phe Ile Ala Ser Asp Met	942
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265 270 275	
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280 285 290	
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295 300 305 310	

aca att gac gga ggg atg gta atg taagatttga gttagcttga tgcacttcta 1140
 Thr Ile Asp Gly Gly Met Val Met
 315

cttttgcgtga gcatttaattg ttgaacacccc ttgttgtgca cgggcgattt tggacaacaa 1200
 attagtgttg tctctttctt tgtaatactc tctggtaata aatctagcat gtggaatgga 1260
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 35 40 45
 Gly Arg Gly Phe Ser Gly Val Gln Thr His Val Ala Ala Val Glu Gln
 50 55 60
 Ala Val Val Lys Asp Ala Thr Lys Leu Glu Ala Pro Val Val Val Val
 65 70 75 80
 Thr Gly Ala Ser Arg Gly Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly
 85 90 95
 Lys Ala Gly Cys Lys Val Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu
 100 105 110
 Ala Glu Glu Val Ser Lys Glu Ile Glu Ala Ser Gly Gly Glu Ala Ile
 115 120 125
 Thr Phe Gly Gly Asp Val Ser Lys Glu Ala Asp Val Glu Ser Met Met
 130 135 140
 Lys Ala Ala Leu Asp Lys Trp Gly Thr Ile Asp Val Leu Val Asn Asn
 145 150 155 160
 Ala Gly Ile Thr Arg Asp Thr Leu Leu Met Arg Met Lys Lys Ser Gln
 165 170 175
 Trp Gln Asp Val Ile Asp Leu Asn Leu Thr Gly Val Phe Leu Cys Thr
 180 185 190
 Gln Ala Ala Thr Lys Val Met Met Lys Lys Arg Lys Gly Lys Ile Ile
 195 200 205
 Asn Ile Ala Ser Val Val Gly Leu Thr Gly Asn Val Gly Gln Ala Asn
 210 215 220
 Tyr Ser Ala Ala Lys Ala Gly Val Ile Gly Phe Thr Lys Thr Val Ala
 225 230 235 240
 Arg Glu Tyr Ala Ser Arg Asn Ile Asn Val Asn Ala Ile Ala Pro Gly
 245 250 255
 Phe Ile Ala Ser Asp Met Thr Ala Glu Leu Gly Glu Glu Leu Glu Lys
 260 265 270
 Lys Ile Leu Ser Thr Ile Pro Leu Gly Arg Tyr Gly Gln Pro Glu Glu
 275 280 285
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 Met
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gcc gct gcc aca gcc gcc gcc gcc gcg ctc gcc tcc ccg gcg ggc ctc 165
 Ala Ala Ala Thr Ala Ala Ala Ala Leu Ala Ser Pro Ala Gly Leu
 5 10 15

tcc aca tcg ctg gcg cgc cgc gcc ctc gtc agc ttc gca ccc gcg ctc 213
 Ser Thr Ser Leu Ala Arg Arg Gly Leu Val Ser Phe Ala Pro Ala Leu
 20 25 30

cgc ccc gcc cct gac cgc agc tct cgc gcc gtc gcc ctc ctc ggt gta 261
 Arg Pro Gly Pro Asp Arg Ser Ser Arg Ala Val Ala Leu Leu Gly Val
 35 40 45

cga act cat gtc acg gct gtt gat caa gcc att gta aaa ggt gat aca 309
 Arg Thr His Val Thr Ala Val Asp Gln Ala Ile Val Lys Gly Asp Thr
 50 55 60 65

aag ttg gaa ggt cct gtg gtt gtt gtt act ggt gct tcc agg ggg att 357
 Lys Leu Glu Gly Pro Val Val Val Val Thr Gly Ala Ser Arg Gly Ile
 70 75 80

gga aaa gcc act gca ttg gct ctt gga aaa gca gcc tgc aag gtc ttg 405
 Gly Lys Ala Thr Ala Leu Ala Leu Gly Lys Ala Gly Cys Lys Val Leu
 85 90 95

gtg aat tat gct cga tct tca aag gag gct gaa gaa gtc tcc aag gag 453
 Val Asn Tyr Ala Arg Ser Ser Lys Glu Ala Glu Glu Val Ser Lys Glu
 100 105 110

att gaa gca tct gga gcc cag gcc att acc ttt gga gga gat gtt tcc 501
 Ile Glu Ala Ser Gly Gln Ala Ile Thr Phe Gly Gly Asp Val Ser
 115 120 125

aaa gag gct gat gtt gaa tct atg ata aaa gtg gct gtt gat aca tgg 549
 Lys Glu Ala Asp Val Glu Ser Met Ile Lys Val Ala Val Asp Thr Trp
 130 135 140 145

gga acg att gat gta cta gta aat aat gca gga atc aca cgg gac aca 597
 Gly Thr Ile Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Thr
 150 155 160

ttg ttg atg aga atg aag aaa tca cag tgg caa gat gcg att gat ttg 645
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165

170

175

aat ctt aca ggc gtt ttc ctt tgc acg cag gct gca aca aaa gta atg 693
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atg aag aag aaa aag gga aga att atc aat ata gca tgc gtt gtt ggt 741
 Met Lys Lys Lys Lys Gly Arg Ile Ile Asn Ile Ala Ser Val Val Gly
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ctt act ggt aat gct gga caa gct aat tat gct gct gcc aag gct ggg 789
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 210 215 220 225

gtt att ggg ttc aca aaa aca gtt gct agg gag tat gcc agc aga aat 837
 Val Ile Gly Phe Thr Lys Thr Val Ala Arg Glu Tyr Ala Ser Arg Asn
 230 235 240

att aat gca aac gtt atc gct cct gga ttt att gct tca gat atg act 885
 Ile Asn Ala Asn Val Ile Ala Pro Gly Phe Ile Ala Ser Asp Met Thr
 245 250 255

gct gaa ctt ggt gaa gag tta gag aag aaa att ctg tca act att cct 933
 Ala Glu Leu Gly Glu Glu Leu Glu Lys Lys Ile Leu Ser Thr Ile Pro
 260 265 270

tta ggg cgc tat ggt cgg cca gag gat gta gca ggc ctg gtg gaa ttc 981
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 275 280 285

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 Ile Asp Gly Gly Met Val Met
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 35 40 45
 Val Arg Thr His Val Thr Ala Val Asp Gln Ala Ile Val Lys Gly Asp
 50 55 60

Thr Lys Leu Glu Gly Pro Val Val Val Val Thr Gly Ala Ser Arg Gly
65 70 75 80
Ile Gly Lys Ala Thr Ala Leu Ala Leu Gly Lys Ala Gly Cys Lys Val
85 90 95
Leu Val Asn Tyr Ala Arg Ser Ser Lys Glu Ala Glu Glu Val Ser Lys
100 105 110
Glu Ile Glu Ala Ser Gly Gly Gln Ala Ile Thr Phe Gly Gly Asp Val
115 120 125
Ser Lys Glu Ala Asp Val Glu Ser Met Ile Lys Val Ala Val Asp Thr
130 135 140
Trp Gly Thr Ile Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp
145 150 155 160
Thr Leu Leu Met Arg Met Lys Lys Ser Gln Trp Gln Asp Ala Ile Asp
165 170 175
Leu Asn Leu Thr Gly Val Phe Leu Cys Thr Gln Ala Ala Thr Lys Val
180 185 190
Met Met Lys Lys Lys Gly Arg Ile Ile Asn Ile Ala Ser Val Val
195 200 205
Gly Leu Thr Gly Asn Ala Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala
210 215 220
Gly Val Ile Gly Phe Thr Lys Thr Val Ala Arg Glu Tyr Ala Ser Arg
225 230 235 240
Asn Ile Asn Ala Asn Val Ile Ala Pro Gly Phe Ile Ala Ser Asp Met
245 250 255
Thr Ala Glu Leu Gly Glu Glu Leu Glu Lys Lys Ile Leu Ser Thr Ile
260 265 270
Pro Leu Gly Arg Tyr Gly Arg Pro Glu Asp Val Ala Gly Leu Val Glu
275 280 285
Phe Leu Ala Leu Ser Pro Ala Ala Ser Tyr Ile Thr Gly Gln Val Leu
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t atg gct tcc att gcc gga tcc aac tgc gtc gct ctc cga acc gcc aac 169
Met Ala Ser Ile Ala Gly Ser Asn Cys Val Ala Leu Arg Thr Ala Asn
1 5 10 15
ttc ggc gcc tcc ggt aac cgg aaa atc ggc cag atc cgc caa tgg tct 217
Phe Gly Ala Ser Gly Asn Arg Lys Ile Gly Gln Ile Arg Gln Trp Ser
20 25 30
cgg att ctc acg aat ctc cgt ccc gtt tcc ggt ctt cgt cac cga tcg 265
Pro Ile Leu Thr Asn Leu Arg Pro Val Ser Gly Leu Arg His Arg Ser
35 40 45

aat act ccg ttt agc tcc tcc ggt gtg aga gca cag gtt gct act ctg 313
 Asn Thr Pro Phe Ser Ser Gly Val Arg Ala Gln Val Ala Thr Leu
 50 55 60

gag gaa gca gga acc gga gca act cag aaa gtg gaa gcg ccg gtt gca 361
 Glu Glu Ala Gly Thr Gly Ala Thr Gln Lys Val Glu Ala Pro Val Ala
 65 70 75 80

gtg gtg acc gga gct tcc aga ggc att ggc aaa gcg att gca ctg tca 409
 Val Val Thr Gly Ala Ser Arg Gly Ile Gly Lys Ala Ile Ala Leu Ser
 85 90 95

tta ggt aaa gca ggt tgc aag gtt ctg gtc aac tat gca agg tca tcc 457
 Leu Gly Lys Ala Gly Cys Lys Val Leu Val Asn Tyr Ala Arg Ser Ser
 100 105 110

aag gaa gct gag gag gtt tcc aag gag att gag gag ttt ggt ggt caa 505
 Lys Glu Ala Glu Glu Val Ser Lys Glu Ile Glu Glu Phe Gly Gly Gln
 115 120 125

gct ctt aca ttt ggt gga gat gtt tct aac gag gct gat gtg gag tct 553
 Ala Leu Thr Phe Gly Gly Asp Val Ser Asn Glu Ala Asp Val Glu Ser
 130 135 140

atg att aaa act gca gtt gat gct tgg gga aca gtt gat gta tta ata 601
 Met Ile Lys Thr Ala Val Asp Ala Trp Gly Thr Val Asp Val Leu Ile
 145 150 155 160

aac aat gca gga ata aca aga gat ggt tta tta atg aga atg aag aaa 649
 Asn Asn Ala Gly Ile Thr Arg Asp Gly Leu Leu Met Arg Met Lys Lys
 165 170 175

tct caa tgg cag gat gtt att gat cta aat ctc act ggt gtt ttt ctt 697
 Ser Gln Trp Gln Asp Val Ile Asp Leu Asn Leu Thr Gly Val Phe Leu
 180 185 190

tgc aca cag gct gct gct aag att atg atg aag aaa aag aag gga agg 745
 Cys Thr Gln Ala Ala Ala Lys Ile Met Met Lys Lys Lys Gly Arg
 195 200 205

atc gtc aat att gca tca gtt gtt ggt ttg gtt ggc aat gtt gga caa 793
 Ile Val Asn Ile Ala Ser Val Val Gly Leu Val Gly Asn Val Gly Gln
 210 215 220

gcc aat tat agt gct gca aaa gca gga gta att ggc ctg aca aaa act 841
 Ala Asn Tyr Ser Ala Ala Lys Ala Gly Val Ile Gly Leu Thr Lys Thr
 225 230 235 240

ggt gcg aag gaa tat gct agt aga aac atc act gtt aat gca gtt gct 889
 Val Ala Lys Glu Tyr Ala Ser Arg Asn Ile Thr Val Asn Ala Val Ala
 245 250 255

cca ggg ttt att gca tct gac atg act gcc aag cta gga caa gac att 937
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 Arg Thr Lys Gly Pro Gly Arg Ala Arg Lys Val Pro Ser Gln Val Leu
 15 20 25
 gct ttt cag cgt tcc aat tca aat ggt tca ttt ccc tca tca gaa cag 147
 Ala Phe Gln Arg Ser Asn Ser Asn Gly Ser Phe Pro Ser Ser Glu Gln
 30 35 40
 cta gaa ctt gaa gca agc cag aag aac atg gaa gca cct gtt gtt gta 195
 Leu Glu Leu Glu Ala Ser Gln Lys Asn Met Glu Ala Pro Val Val Val
 45 50 55 60
 gtc act gga gcc tcc aga ggc att ggc cgt gca att gca ctt tcc ttg 243
 Val Thr Gly Ala Ser Arg Gly Ile Gly Arg Ala Ile Ala Leu Ser Leu
 65 70 75
 ggt aaa gcc cca tgc aag gtg ttg gtc aac tat gcc agg tca tcc atg 291
 Gly Lys Ala Pro Cys Lys Val Leu Val Asn Tyr Ala Arg Ser Ser Met
 80 85 90
 caa gct gag gag gtt tcc aac ttg att gag gcg ttt ggt gga caa gct 339
 Gln Ala Glu Glu Val Ser Asn Leu Ile Glu Ala Phe Gly Gly Gln Ala
 95 100 105
 ctt acc ttc gag gga gat gtt tca aat gag gcc gat gtg gaa tct atg 387
 Leu Thr Phe Glu Gly Asp Val Ser Asn Glu Ala Asp Val Glu Ser Met
 110 115 120
 att aga act gca gtt gat gct tgg gga act gtt gat gta ttg gta aac 435
 Ile Arg Thr Ala Val Asp Ala Trp Gly Thr Val Asp Val Leu Val Asn
 125 130 135 140
 aat gca gga att act cga gat ggt ttg tta atg aga atg aag aaa tca 483

Asn Ala Gly Ile Thr Arg Asp Gly Leu Leu Met Arg Met Lys Lys Ser
 145 150 155
 caa tgg cag gaa gtt att gat ctg aat ctc act ggt gtt ttt ctt tgc 531
 Gln Trp Gln Glu Val Ile Asp Leu Asn Leu Thr Gly Val Phe Leu Cys
 160 165 170
 atg cag gca gca gca aag att atg acg atg aaa aag aag gga agg ata 579
 Met Gln Ala Ala Ala Lys Ile Met Thr Met Lys Lys Lys Gly Arg Ile
 175 180 185
 atc aat att aca tca gtt att ggt cag gtt ggc aat gtt gga caa gcc 627
 Ile Asn Ile Thr Ser Val Ile Gly Gln Val Gly Asn Val Gly Gln Ala
 190 195 200
 aat tat agt gct gca aag gca ggg gta att ggc ctc aca aaa agt gct 675
 Asn Tyr Ser Ala Ala Lys Ala Gly Val Ile Gly Leu Thr Lys Ser Ala
 205 210 215 220
 gcc agg gaa tat gct agc aga aac atc act gtt aat gca gta gcc cct 723
 Ala Arg Glu Tyr Ala Ser Arg Asn Ile Thr Val Asn Ala Val Ala Pro
 225 230 235
 ggg ttt att gca tct gat atg act gcc aat cta cga cca ggc att gag 771
 Gly Phe Ile Ala Ser Asp Met Thr Ala Asn Leu Arg Pro Gly Ile Glu
 240 245 250
 aaa aaa aga ttg gaa tta atc ccc tta gga aga ctt ggc caa cca gaa 819
 Lys Lys Arg Leu Glu Leu Ile Pro Leu Gly Arg Leu Gly Gln Pro Glu
 255 260 265
 gaa gtt gct gga ctt gtg gaa ttc ttg gct ctt aat cct gct gcc aat 867
 Glu Val Ala Gly Leu Val Glu Phe Leu Ala Leu Asn Pro Ala Ala Asn
 270 275 280
 tac atc act ggg cag gtg ttc acc att gat gga ggt ttg gca atg 912
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 285 290 295
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35 40 45
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 Ser Arg Gly Ile Gly Arg Ala Ile Ala Leu Ser Leu Gly Lys Ala Pro
 65 70 75 80
 Cys Lys Val Leu Val Asn Tyr Ala Arg Ser Ser Met Gln Ala Glu Glu
 85 90 95
 Val Ser Asn Leu Ile Glu Ala Phe Gly Gly Gln Ala Leu Thr Phe Glu
 100 105 110
 Gly Asp Val Ser Asn Glu Ala Asp Val Glu Ser Met Ile Arg Thr Ala
 115 120 125
 Val Asp Ala Trp Gly Thr Val Asp Val Leu Val Asn Asn Ala Gly Ile
 130 135 140
 Thr Arg Asp Gly Leu Leu Met Arg Met Lys Lys Ser Gln Trp Gln Glu
 145 150 155 160
 Val Ile Asp Leu Asn Leu Thr Gly Val Phe Leu Cys Met Gln Ala Ala
 165 170 175
 Ala Lys Ile Met Thr Met Lys Lys Lys Gly Arg Ile Ile Asn Ile Thr
 180 185 190
 Ser Val Ile Gly Gln Val Gly Asn Val Gly Gln Ala Asn Tyr Ser Ala
 195 200 205
 Ala Lys Ala Gly Val Ile Gly Leu Thr Lys Ser Ala Ala Arg Glu Tyr
 210 215 220
 Ala Ser Arg Asn Ile Thr Val Asn Ala Val Ala Pro Gly Phe Ile Ala
 225 230 235 240
 Ser Asp Met Thr Ala Asn Leu Arg Pro Gly Ile Glu Lys Lys Arg Leu
 245 250 255
 Glu Leu Ile Pro Leu Gly Arg Leu Gly Gln Pro Glu Glu Val Ala Gly
 260 265 270
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 275 280 285
 Gln Val Phe Thr Ile Asp Gly Gly Leu Ala Met
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<210> 9
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 <212> DNA
 <213> *Pseudomonas fluorescens*

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 <222> (1)...(1680)
 <223> SEQ ID NO:1 from WO 01/23580

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 aaaaacgttc tgctcggttc ttcgcccttg cagccggaag ccgacgacgg tcgtctcgg 240
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 cggcgccggg tgaagcgctt cttcgaaacc ggccggaaga gctgtctcga cggcctctcg 480
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 ctggagctga tccagtacaa gcccatcacc gagcaggtgc acgagcgccc gctgctggtg 660

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gccacgcgcg	aatggggcct	gtcgacctac	atcgaggcgc	tcaaggaaac	ctcagagggtg	840
gtgctggaag	tcacgggcgc	caaggaccct	aacatgctcg	gtgcctgctc	cggcggcctc	900
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